

03CO

0000288

O/PE

CRF Errors Corrected by the STIC Systems Branch

CRF Processing Date: 12/17/2001

Edited by: AS

Verified by: AS

(STIC stat)

Serial Number: 10/002,854

ENTERED
#4

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/lastname at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☒ Other: Seq 2 - corrected amino acid numbering

Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

OIPE

RAW SEQUENCE LISTING

DATE: 12/17/2001

PATENT APPLICATION: US/10/002,854

TIME: 20:19:56

Input Set : A:\Pto.amc

Output Set: N:\CRF3\12172001\J002854.raw

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4 <110> APPLICANT: Scadden, David T.
5   Poznansky, Mark C.
6   Olszak, Ivona T.
7   Brown, Edward M.
9 <120> TITLE OF INVENTION: THE CaR RECEPTOR AS A MEDIATOR OF
10  MIGRATORY CELL CHEMOTAXIS AND/OR CHEMOKINESIS
13 <130> FILE REFERENCE: M0765/7038/ERG/KA
C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/002,854
C--> 15 <141> CURRENT FILING DATE: 2001-11-01
15 <150> PRIOR APPLICATION NUMBER: PCT/US00/15440
16 <151> PRIOR FILING DATE: 2000-06-02
18 <160> NUMBER OF SEQ ID NOS: 2
20 <170> SOFTWARE: FastSEQ for Windows Version 3.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 3361
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (29)...(3262)
30 <223> OTHER INFORMATION: Ca-sensing Receptor
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33  tcccttgccc tggagagacg gcagaacc atg gca ttt tat agc tgc tgc tgg      52
34                               Met Ala Phe Tyr Ser Cys Cys Trp
35                               1           5
37  gtc ctc ttg gca ctc acc tgg cac acc tct gcc tac ggg cca gac cag      100
38  Val Leu Leu Ala Leu Thr Trp His Thr Ser Ala Tyr Gly Pro Asp Gln
39      10           15           20
41  cga gcc caa aag aag ggg gac att atc ctt ggg ggg ctc ttt cct att      148
42  Arg Ala Gln Lys Lys Gly Asp Ile Ile Leu Gly Gly Leu Phe Pro Ile
43      25           30           35           40
45  cat ttt gga gta gca gct aaa gat caa gat ctc aaa tca agg ccg gag      196
46  His Phe Gly Val Ala Ala Lys Asp Gln Asp Leu Lys Ser Arg Pro Glu
47      45           50           55
49  tct gtg gaa tgt atc agg tat aat ttc cgt ggg ttt cgc tgg tta cag      244
50  Ser Val Glu Cys Ile Arg Tyr Asn Phe Arg Gly Phe Arg Trp Leu Gln
51      60           65           70
53  gct atg ata ttt gcc ata gag gag ata aac agc agc cca gcc ctt ctt      292
54  Ala Met Ile Phe Ala Ile Glu Glu Ile Asn Ser Ser Pro Ala Leu Leu
55      75           80           85
57  ccc aac ttg acg ctg gga tac agg ata ttt gac act tgc aac acc gtt      340
58  Pro Asn Leu Thr Leu Gly Tyr Arg Ile Phe Asp Thr Cys Asn Thr Val
59      90           95           100
61  tct aag gcc ttg gaa gcc acc ctg agt ttt gtt gct caa aac aaa att      388
62  Ser Lys Ala Leu Glu Ala Thr Leu Ser Phe Val Ala Gln Asn Lys Ile
63      105           110           115           120
65  gat tct ttg aac ctt gat gag ttc tgc aac tgc tca gag cac att ccc      436

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66  Asp Ser Leu Asn Leu Asp Glu Phe Cys Asn Cys Ser Glu His Ile Pro
67              125              130              135
69  tct acg att gct gtg gtg gga gca act ggc tca ggc gtc tcc acg gca      484
70  Ser Thr Ile Ala Val Val Gly Ala Thr Gly Ser Gly Val Ser Thr Ala
71              140              145              150
73  gtg gca aat ctg ctg ggg ctc ttc tac att ccc cag gtc agt tat gcc      532
74  Val Ala Asn Leu Leu Gly Leu Phe Tyr Ile Pro Gln Val Ser Tyr Ala
75              155              160              165
77  tcc tcc agc aga ctc ctc agc aac aag aat caa ttc aag tct ttc ctc      580
78  Ser Ser Ser Arg Leu Leu Ser Asn Lys Asn Gln Phe Lys Ser Phe Leu
79              170              175              180
81  cga acc atc ccc aat gat gag cac cag gcc act gcc atg gca gac atc      628
82  Arg Thr Ile Pro Asn Asp Glu His Gln Ala Thr Ala Met Ala Asp Ile
83  185              190              195              200
85  atc gag tat ttc cgc tgg aac tgg gtg ggc aca att gca gct gat gac      676
86  Ile Glu Tyr Phe Arg Trp Asn Trp Val Gly Thr Ile Ala Ala Asp Asp
87              205              210              215
89  gac tat ggg cgg ccg ggg att gag aaa ttc cga gag gaa gct gag gaa      724
90  Asp Tyr Gly Arg Pro Gly Ile Glu Lys Phe Arg Glu Glu Ala Glu Glu
91              220              225              230
93  agg gat atc tgc atc gac ttc agt gaa ctc atc tcc cag tac tct gat      772
94  Arg Asp Ile Cys Ile Asp Phe Ser Glu Leu Ile Ser Gln Tyr Ser Asp
95              235              240              245
97  gag gag gag atc cag cat gtg gta gag gtg att caa aat tcc acg gcc      820
98  Glu Glu Glu Ile Gln His Val Val Glu Val Ile Gln Asn Ser Thr Ala
99              250              255              260
101  aaa gtc atc gtg gtt ttc tcc agt ggc cca gat ctt gag ccc ctc atc      868
102  Lys Val Ile Val Val Phe Ser Ser Gly Pro Asp Leu Glu Pro Leu Ile
103  265              270              275              280
105  aag gag att gtc cgg cgc aat atc acg ggc aag atc tgg ctg gcc agc      916
106  Lys Glu Ile Val Arg Arg Asn Ile Thr Gly Lys Ile Trp Leu Ala Ser
107              285              290              295
109  gag gcc tgg gcc agc tcc tcc ctg atc gcc atg cct cag tac ttc cac      964
110  Glu Ala Trp Ala Ser Ser Ser Leu Ile Ala Met Pro Gln Tyr Phe His
111              300              305              310
113  gtg gtt ggc ggc acc att gga ttc gct ctg aag gct ggg cag atc cca      1012
114  Val Val Gly Gly Thr Ile Gly Phe Ala Leu Lys Ala Gly Gln Ile Pro
115              315              320              325
117  ggc ttc cgg gaa ttc ctg aag aag gtc cat ccc agg aag tct gtc cac      1060
118  Gly Phe Arg Glu Phe Leu Lys Lys Val His Pro Arg Lys Ser Val His
119              330              335              340
121  aat ggt ttt gcc aag gag ttt tgg gaa gaa aca ttt aac tgc cac ctc      1108
122  Asn Gly Phe Ala Lys Glu Phe Trp Glu Glu Thr Phe Asn Cys His Leu
123  345              350              355              360
125  caa gaa ggt gca aaa gga cct tta cct gtg gac acc ttt ctg aga ggt      1156
126  Gln Glu Gly Ala Lys Gly Pro Leu Pro Val Asp Thr Phe Leu Arg Gly
127              365              370              375
129  cac gaa gaa agt ggc gac agg ttt agc aac agc tcg aca gcc ttc cga      1204
130  His Glu Glu Ser Gly Asp Arg Phe Ser Asn Ser Ser Thr Ala Phe Arg

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131		380		385		390		
133	ccc ctc tgt aca ggg gat gag aac atc agc agt gtc gag acc cct tac							1252
134	Pro Leu Cys Thr Gly Asp Glu Asn Ile Ser Ser Val Glu Thr Pro Tyr							
135		395		400		405		
137	ata gat tac acg cat tta cgg ata tcc tac aat gtg tac tta gca gtc							1300
138	Ile Asp Tyr Thr His Leu Arg Ile Ser Tyr Asn Val Tyr Leu Ala Val							
139		410		415		420		
141	tac tcc att gcc cac gcc ttg caa gat ata tat acc tgc tta cct ggg							1348
142	Tyr Ser Ile Ala His Ala Leu Gln Asp Ile Tyr Thr Cys Leu Pro Gly							
143		425		430		435		440
145	aga ggg ctc ttc acc aat ggc tcc tgt gca gac atc aag aaa gtt gag							1396
146	Arg Gly Leu Phe Thr Asn Gly Ser Cys Ala Asp Ile Lys Lys Val Glu							
147		445		450		455		
149	gcg tgg cag gtc ctg aag cac cta cgg cat cta aac ttt aca aac aat							1444
150	Ala Trp Gln Val Leu Lys His Leu Arg His Leu Asn Phe Thr Asn Asn							
151		460		465		470		
153	atg ggg gag cag gtg acc ttt gat gag tgt ggt gac ctg gtg ggg aac							1492
154	Met Gly Glu Gln Val Thr Phe Asp Glu Cys Gly Asp Leu Val Gly Asn							
155		475		480		485		
157	tat tcc atc atc aac tgg cac ctc tcc cca gag gat ggc tcc atc gtg							1540
158	Tyr Ser Ile Ile Asn Trp His Leu Ser Pro Glu Asp Gly Ser Ile Val							
159		490		495		500		
161	ttt aag gaa gtc ggg tat tac aac gtc tat gcc aag aag gga gaa aga							1588
162	Phe Lys Glu Val Gly Tyr Tyr Asn Val Tyr Ala Lys Lys Gly Glu Arg							
163		505		510		515		520
165	ctc ttc atc aac gag gag aaa atc ctg tgg agt ggg ttc tcc agg gag							1636
166	Leu Phe Ile Asn Glu Glu Lys Ile Leu Trp Ser Gly Phe Ser Arg Glu							
167		525		530		535		
169	gtg ccc ttc tcc aac tgc agc cga gac tgc ctg gca ggg acc agg aaa							1684
170	Val Pro Phe Ser Asn Cys Ser Arg Asp Cys Leu Ala Gly Thr Arg Lys							
171		540		545		550		
173	ggg atc att gag ggg gag ccc acc tgc tgc ttt gag tgt gtg gag tgt							1732
174	Gly Ile Ile Glu Gly Glu Pro Thr Cys Cys Phe Glu Cys Val Glu Cys							
175		555		560		565		
177	cct gat ggg gag tat agt gat gag aca gat gcc agt gcc tgt aac aag							1780
178	Pro Asp Gly Glu Tyr Ser Asp Glu Thr Asp Ala Ser Ala Cys Asn Lys							
179		570		575		580		
181	tgc cca gat gac ttc tgg tcc aat gag aac cac acc tcc tgc att gcc							1828
182	Cys Pro Asp Asp Phe Trp Ser Asn Glu Asn His Thr Ser Cys Ile Ala							
183		585		590		595		600
185	aag gag atc gag ttt ctg tgc tgg acg gag ccc ttt ggg atc gca ctc							1876
186	Lys Glu Ile Glu Phe Leu Ser Trp Thr Glu Pro Phe Gly Ile Ala Leu							
187		605		610		615		
189	acc ctc ttt gcc gtg ctg ggc att ttc ctg aca gcc ttt gtg ctg ggt							1924
190	Thr Leu Phe Ala Val Leu Gly Ile Phe Leu Thr Ala Phe Val Leu Gly							
191		620		625		630		
193	gtg ttt atc aag ttc cgc aac aca ccc att gtc aag gcc acc aac cga							1972
194	Val Phe Ile Lys Phe Arg Asn Thr Pro Ile Val Lys Ala Thr Asn Arg							
195		635		640		645		

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197	gag	ctc	tcc	tac	ctc	ctc	ctc	ttc	tcc	ctg	ctc	tgc	tgc	ttc	tcc	agc	2020
198	Glu	Leu	Ser	Tyr	Leu	Leu	Leu	Phe	Ser	Leu	Leu	Cys	Cys	Phe	Ser	Ser	
199		650						655				660					
201	tcc	ctg	ttc	ttc	atc	ggg	gag	ccc	cag	gac	tgg	acg	tgc	cgc	ctg	cgc	2068
202	Ser	Leu	Phe	Phe	Ile	Gly	Pro	Gln	Asp	Trp	Thr	Cys	Arg	Leu	Arg		
203	665					670				675						680	
205	cag	ccg	gcc	ttt	ggc	atc	agc	ttc	gtg	ctc	tgc	atc	tca	tgc	atc	ctg	2116
206	Gln	Pro	Ala	Phe	Gly	Ile	Ser	Phe	Val	Leu	Cys	Ile	Ser	Cys	Ile	Leu	
207					685					690						695	
209	gtg	aaa	acc	aac	cgt	gtc	ctc	ctg	gtg	ttt	gag	gcc	aag	atc	ccc	acc	2164
210	Val	Lys	Thr	Asn	Arg	Val	Leu	Leu	Val	Phe	Glu	Ala	Lys	Ile	Pro	Thr	
211				700					705					710			
213	agc	ttc	cac	cgc	aag	tgg	tgg	ggg	ctc	aac	ctg	cag	ttc	ctg	ctg	gtt	2212
214	Ser	Phe	His	Arg	Lys	Trp	Trp	Gly	Leu	Asn	Leu	Gln	Phe	Leu	Leu	Val	
215			715					720					725				
217	ttc	ctc	tgc	acc	ttc	atg	cag	att	gtc	atc	tgt	gtg	atc	tgg	ctc	tac	2260
218	Phe	Leu	Cys	Thr	Phe	Met	Gln	Ile	Val	Ile	Cys	Val	Ile	Trp	Leu	Tyr	
219		730					735					740					
221	acc	cgc	ccc	ccc	tca	agc	tac	cgc	aac	cag	gag	ctg	gag	gat	gag	atc	2308
222	Thr	Ala	Pro	Pro	Ser	Ser	Tyr	Arg	Asn	Gln	Glu	Leu	Glu	Asp	Glu	Ile	
223	745					750					755					760	
225	atc	ttc	atc	acg	tgc	cac	gag	ggc	tcc	ctc	atg	gcc	ctg	ggc	ttc	ctg	2356
226	Ile	Phe	Ile	Thr	Cys	His	Glu	Gly	Ser	Leu	Met	Ala	Leu	Gly	Phe	Leu	
227					765				770							775	
229	atc	ggc	tac	acc	tgc	ctg	ctg	gct	gcc	atc	tgc	ttc	ttc	ttt	gcc	ttc	2404
230	Ile	Gly	Tyr	Thr	Cys	Leu	Leu	Ala	Ala	Ile	Cys	Phe	Phe	Phe	Ala	Phe	
231				780					785							790	
233	aag	tcc	cgg	aag	ctg	ccg	gag	aac	ttc	aat	gaa	gcc	aag	ttc	atc	acc	2452
234	Lys	Ser	Arg	Lys	Leu	Pro	Glu	Asn	Phe	Asn	Glu	Ala	Lys	Phe	Ile	Thr	
235			795					800					805				
237	ttc	agc	atg	ctc	atc	ttc	ttc	atc	gtc	tgg	atc	tcc	ttc	att	cca	gcc	2500
238	Phe	Ser	Met	Leu	Ile	Phe	Phe	Ile	Val	Trp	Ile	Ser	Phe	Ile	Pro	Ala	
239		810					815					820					
241	tat	gcc	agc	acc	tat	ggc	aag	ttt	gtc	tct	gcc	gta	gag	gtg	att	gcc	2548
242	Tyr	Ala	Ser	Thr	Tyr	Gly	Lys	Phe	Val	Ser	Ala	Val	Glu	Val	Ile	Ala	
243	825					830					835					840	
245	atc	ctg	gca	gcc	agc	ttt	ggc	ttg	ctg	gcg	tgc	atc	ttc	ttc	aac	aag	2596
246	Ile	Leu	Ala	Ala	Ser	Phe	Gly	Leu	Leu	Ala	Cys	Ile	Phe	Phe	Asn	Lys	
247					845					850						855	
249	acc	tac	atc	att	ctc	ttc	aag	cca	tcc	cgc	aac	acc	atc	gag	gag	gtg	2644
250	Thr	Tyr	Ile	Ile	Leu	Phe	Lys	Pro	Ser	Arg	Asn	Thr	Ile	Glu	Glu	Val	
251				860					865					870			
253	cgt	tgc	agc	acc	gca	cgt	cac	gct	ttc	aag	gtg	gct	gcc	cgg	gcc	acg	2692
254	Arg	Cys	Ser	Thr	Ala	Arg	His	Ala	Phe	Lys	Val	Ala	Ala	Arg	Ala	Thr	
255			875					880					885				
257	ctg	cgc	cgc	agc	aac	gtc	tcc	cgc	aag	cgg	tcc	agc	agc	ctt	gga	ggc	2740
258	Leu	Arg	Arg	Ser	Asn	Val	Ser	Arg	Lys	Arg	Ser	Ser	Ser	Leu	Gly	Gly	
259		890					895					900					
261	tcc	acg	gga	tcc	acc	ccc	tcc	tcc	tcc	atc	agc	agc	aag	agc	aac	agc	2788

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262 Ser Thr Gly Ser Thr Pro Ser Ser Ser Ile Ser Ser Lys Ser Asn Ser
263 905                      910                      915                      920
265 gaa gac cca ttc cca cag ccc gag agg cag aag cag cag cag ccg ctg      2836
266 Glu Asp Pro Phe Pro Gln Pro Glu Arg Gln Lys Gln Gln Gln Pro Leu
267                      925                      930                      935
269 gcc cta acc cag caa gag cag cag cag cag ccc ctg acc ctc cca cag      2884
270 Ala Leu Thr Gln Gln Glu Gln Gln Gln Gln Pro Leu Thr Leu Pro Gln
271                      940                      945                      950
273 cag caa cga tct cag cag cag ccc aga tgc aag cag aag gtc atc ttt      2932
274 Gln Gln Arg Ser Gln Gln Gln Pro Arg Cys Lys Gln Lys Val Ile Phe
275                      955                      960                      965
277 ggc agc ggc acg gtc acc ttc tca ctg agc ttt gat gag cct cag aag      2980
278 Gly Ser Gly Thr Val Thr Phe Ser Leu Ser Phe Asp Glu Pro Gln Lys
279                      970                      975                      980
281 aac gcc atg gcc cac agg aat tct acg cac cag aac tcc ctg gag gcc      3028
282 Asn Ala Met Ala His Arg Asn Ser Thr His Gln Asn Ser Leu Glu Ala
283 985                      990                      995                      1000
285 cag aaa agc agc gat acg ctg acc cga cac cag cca tta ctc ccg ctg      3076
286 Gln Lys Ser Ser Asp Thr Leu Thr Arg His Gln Pro Leu Leu Pro Leu
287                      1005                      1010                      1015
289 cag tgc ggg gaa acg gac tta gat ctg acc gtc cag gaa aca ggt ctg      3124
290 Gln Cys Gly Glu Thr Asp Leu Asp Leu Thr Val Gln Glu Thr Gly Leu
291                      1020                      1025                      1030
293 caa gga cct gtg ggt gga gac cag cgg cca gag gtg gag gac cct gaa      3172
294 Gln Gly Pro Val Gly Gly Asp Gln Arg Pro Glu Val Glu Asp Pro Glu
295                      1035                      1040                      1045
297 gag ttg tcc cca gca ctt gta gtg tcc agt tca cag agc ttt gtc atc      3220
298 Glu Leu Ser Pro Ala Leu Val Val Ser Ser Ser Gln Ser Phe Val Ile
299                      1050                      1055                      1060
301 agt ggt gga ggc agc act gtt aca gaa aac gta gtg aat tca      3262
302 Ser Gly Gly Gly Ser Thr Val Thr Glu Asn Val Val Asn Ser
303 1065                      1070                      1075
305 taaaatggaa ggagaagact gggctaggga gaatgcagag aggtttcttg ggggtcccagg      3322
306 gatgaggaat cgccccagac tcctttcctc tgaggaaga      3361
308 <210> SEQ ID NO: 2
309 <211> LENGTH: 1078
310 <212> TYPE: PRT
311 <213> ORGANISM: Homo sapiens
313 <220> FEATURE:
314 <221> NAME/KEY: PEPTIDE
315 <222> LOCATION: (1)...(1078)
316 <223> OTHER INFORMATION: Ca-sensing Receptor
318 <400> SEQUENCE: 2
319 Met Ala Phe Tyr Ser Cys Cys Trp Val Leu Leu Ala Leu Thr Trp His
320 1 5 10 15
321 Thr Ser Ala Tyr Gly Pro Asp Gln Arg Ala Gln Lys Lys Gly Asp Ile
322 20 25 30
323 Ile Leu Gly Gly Leu Phe Pro Ile His Phe Gly Val Ala Ala Lys Asp
324 35 40 45

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/002,854

DATE: 12/17/2001

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Input Set : A:\Pto.amc

Output Set: N:\CRF3\12172001\J002854.raw

L:15 M:270 C: Current Application Number differs, Replaced Current Application No

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date